



XX W09210519-A.  
XX 25-JUN-1992.  
XX 26-NOV-1991; 91WO-US08889.  
XX 28-NOV-1990; 90AU-0003594.  
XX (LUDM-) LUDMIG INST CANCER RES.  
XX Harpur A, Wilks AF, Ziemlecki A;  
XX WPI; 1992-234591/28.  
XX P-PSDB; R25141.  
XX Novel protein tyrosine kinase mol. - comprises multiple catalytic  
XX domains but no SH2 domain and is for phosphorylation of proteins  
XX  
XX Claim 10; Fig 8; 50pp; English.

This sequence encodes the murine protein tyrosine kinase JAK2 (from  
CC Janus kinase). Northern analysis of JAK2 expression in a mouse  
CC demonstrated the presence of two mRNA transcripts (4.8 and 4.4 kb).  
CC The levels of these transcripts alter with respect to one another in  
CC different tissues. The kidney, spleen and lung appear to express  
CC predominantly the larger form, whereas ovary, placenta, skeletal muscle  
CC and all murine cell lines analysed express both forms at equal levels.  
CC The difference in sizes may be due to differential polyadenylation  
CC sites. Both JAK2 and JAK1 are examples of a new subfamily or class  
CC of protein tyrosine kinase. These can be used in the phosphorylation  
CC of proteins, inhibitors of JAKs and in the design of analogues,  
CC antagonists and agonists of JAK's.

Sequence 3473 BP: 1128 A; 677 C; 781 G; 887 T; 0 other;

alignment\_scores:  
Quality: 2376.50 Length: 984  
Ratio: 3.242 Gaps: 14  
Percent Similarity: 74.492 Percent Identity: 49.695

alignment\_block:  
US-09-397-967-16 x Q25307 ..

Align seg 1/1 to: Q25307 from: 1 to: 3473

128 ILEUASPHEUHIHISVALLLEUHLISLEUPHEALAGINHSARGSERAS 144  
:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |  
1 CTGCTTGATGACTTTGTCACTGCTTACCTTTTGTTCAGTGGCGGCAATGA 50  
144 PLEUVALSERGLYARGLEUPROVALIGLYLEUSERMETLYSGULGNLYG 161  
:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |  
51 TTTTGTCACGATGATGATAAAGACCTGATGCTCATGACATGACATGAGAA 100  
161 IUPHEUSERLEUALAVALLEUASPHEUALAGINMETALARGGLN 177  
|| |:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |  
101 AGTGTCTGGGATGGCGGTGTATGACATGATGACATGATGATGACGAGAAA 150  
178 ALAGINATGPROGLYGLULEULEULYSHYVALSERLYTYSALACYSLE 194  
|| |:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |  
151 GACCGAGCTCCACTGGCTGTCTATGACTGTCTGACGCTACAGACATCTT 200  
194 UPROBROSERLEUARGLASPVALLIEGLINGLYGLINSPHEVALTHIRGA 211  
|| |:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |  
201 ACCAAGATGCGTTCGACGCAAGATCCAGATACATACATTTTAAACCGGA 250  
211 TGAAGTLEARGTARGTTHVALVALLEUALALEULEUPROCYSGLYARGLEU 227  
:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |  
251 AGCGAATCAGATGATTCGACATTCATTCAGCAATTCAGCAATTCAGCAAT 300  
228 PROGLYARGPROTYALALEUMETALALYSTYRILEUASPHEUGLYAR 244  
:::||||| |:::||||| |:::||||| |:::||||| |:::||||| |

301 AAGCCACTGCCAGGAACCTTAAACTTATTAACCTGGAAAC 350  
244 GLEUHSIPROALAHATHRGLUHTHRPHEARGVAL..... 256  
|||::: ||| |:::||||| |:::||||| |:::||||| |  
351 CCTGCAGTCCGCTTCTACACAGAACAGTTTGAAGTAAAGAAATCTGCAG 400  
257 ..GLYLEUPROGLYALAGLNGLUUPROGLYLEULEUARGVALALAGLY 272  
|| |:::||||| |:::||||| |:::||||| |:::||||| |  
401 GAGGT...CCTTCAGTGAGAGATTTTTCACACCATTAATTAATCTGA 447  
273 ASPASNGLYLEUPROTPRPSER..... 280  
:::||||| |:::||||| |:::||||| |:::||||| |  
448 AACGCTGAATTCAGTGTACAGAGGAACATAGGAAGTAGACACT 497  
281 ..ASNAPGLLEUPHEGHTHRPHECYASPPHEPROGLUILEVALSPV 297  
:::||||| |:::||||| |:::||||| |:::||||| |  
498 GACAGAACAGAGCGTACATTAATTTGATTTCCGATATTTATGATG 547  
297 ALSERILEASNGLALAPROARGVALIGLYPROALAGLYGLINHSARGLEU 313  
|||:::||||| |:::||||| |:::||||| |:::||||| |  
548 TCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 594  
314 VALTHVALTHIRARGMETASPGLYHISILEUENGLUALAGLUPHEPROGL 330  
|||:::||||| |:::||||| |:::||||| |:::||||| |  
595 TCACTGTCCATTAACAAAGATGTAAGTTTGGAGATGATGATGATG 644  
330 YLEUPROGLUALALEUSERPHEVALALALEUVALASPGLYTHRPHETGL 347  
|||:::||||| |:::||||| |:::||||| |:::||||| |  
645 ATTAATAAACCTGTGATTCGCTCATTAATGACGGGATTAATGAC 694  
347 EUILECYASPPSERARGHISTYRPHECYLSYGLUVALALAPROARG 363  
|| |:::||||| |:::||||| |:::||||| |:::||||| |  
695 TACAGCGGATGCGGACCATTAACCTGCAAGAGGTGCTCCCGACACT 744  
364 LEULEUGLUGLUALASPVALCYSHISGLYPROLEHTHRLEUASP 380  
:::||||| |:::||||| |:::||||| |:::||||| |  
745 GTGCTGAGAACATACACGACACTGCGCCGCAATATCAATGATTT 794  
380 EALAHLEHISLEULYSALALAGLYSERLEUPROGLYTHYRILEL 397  
|||:::||||| |:::||||| |:::||||| |:::||||| |  
795 TCCCATTAACCAATTAAGAGGCGGTATACACGCTGACATATATGCTG 844  
397 EUARGARGSERPROGLINASPTYRASPSPHELEUHTHRALACYSVAL 413  
|||:::||||| |:::||||| |:::||||| |:::||||| |  
845 TACGATGACGCGCTTAAGACTCAACAAATCTTCTACCTTGTCTGCT 894  
414 GLNTHRPROLEUGLYPROASPTYRGLYSGLYSEULEIARGGLINSP 430  
:::||||| |:::||||| |:::||||| |:::||||| |  
895 GAGCGAGAAATGTCATTAATTAATTAACACTGTTGATTAACAAAGA 944  
430 OSERGLYALAPHEUSERLEUVALIGLYLEUSERGLNPROHISARGSER 447  
|||:::||||| |:::||||| |:::||||| |:::||||| |  
945 GATGAGAGATTAACACCTCAGCGGACTAATAGAACTTCACTGATCTTA 994  
447 TGLUULEULEUALALACYSSTRPASNSERGLYLEUARGVALASPGLYLA 463  
:::||||| |:::||||| |:::||||| |:::||||| |  
995 AGGACCTTTGATTAATGCTACAGATGGAAGTGTGCTGACACAGTATC 1044  
464 ALALEUHTYRLEUHTSERCYSAIPROARGPROLYSGLYLYSERAS 480  
|||:::||||| |:::||||| |:::||||| |:::||||| |  
1045 ATCTTCAGATTTTACCAATGCTGCCGCCCAAGCAAAAGATAATCAAA 1094  
480 NLEULIEVALARGARGLYCYSHNSPROMALAPROALAPROGLYCYSS 497  
|||:::||||| |:::||||| |:::||||| |:::||||| |  
1095 CCTTCCTGCTTTCAGA.....ACAATGTATTTCTGATGTTCAAGTCT 1138  
497 ERPROSERCYSAALA.....LEUHTGLNLEUSERPHEHISHTHR 510  
|||:::||||| |:::||||| |:::||||| |:::||||| |  
1139 CACCAACATTAACGAGCATTAATATGTAATCAATCAATGCTGTTTCAAAA 1188  
511 ILEPROTHASPSERLEUGLUTRPHISGLUASNLEUGLYHISGLYSEPH 527  
|||:::||||| |:::||||| |:::||||| |:::||||| |  
1189 ATCAGGAATGAAGATTAATTAATTAATGAAGACTTCCGCAAGACTCTT 1238

527 eThLysIlePheArgGlySerArgGluValAsp... GlyLut 543  
 1229 TACAAAATTTTAAAGGTAAAGAGAGAGATTCGATATGATGTCAC 1288  
 543 hThAspSerGluValIleuLeuLysValMetAspSerArgHisArgAsn 559  
 1289 TGCCAAACCGAAGCTCTTTGAAAGCTCCAGATTAAGCATAAGGAAAC 1338  
 560 CysMetGluSerPheLeuGluAlaAlaSerLeuMetSerGluValSery 576  
 1339 TATTCAGAGCTCTTCTCGAAGCAGCAGCATGATGATCAGCTTCTCA 1388  
 576 rProHisLeuValIleuLeuHisGlyValCysMetAlaGly... AspSeri 592  
 1389 CAAGCATTTGGTTTGAATTATGATGCTCTGCTGAGAGAGAGACAA 1438  
 592 IeMetValGlnGluPheValTyrLeuGlyValAlaIleAspMetTyrLeuArg 608  
 1439 TTCTGCTCAAGATTTGTAAATTTGGATCAGCTGATACATACCTGAG 1488  
 609 LysArgGlyHisLeuValSerAlaSerTyrLysLeuGlnValThrIysG 625  
 1489 AAGAACAAATTCATTAATATATATGAAACTTGAGTGGCTAGCA 1538  
 625 nLeuAlaTyrAlaLeuAsnTyrLeuGluAspLysGlyLeuProHisGly 642  
 1539 GTTGCGATGGCCATGCATTTTCTAGAGAGAAAATCCCTATTGATGGA 1588  
 642 snValSerAlaArgLysValIleuLeuAlaArgLysGly... Asp 656  
 1589 ATGTGTGCTAAATAATATCTGCTTATCAGAGAGAGAGAGAGAGAC 1638  
 657 GlyAsnProProPheIleLysLeuSerAspProGlyValSerProThry 673  
 1639 GGGAGCCACCTTTCATCAAACTAGATCCGCACTAGCATTCACAGT 1688  
 673 IleSerLeuGluMetLeuThrAspArgIleProTyrValAlaProGlnC 690  
 1689 TCTACCCAGAGACATTTCTCAGCAGAGAAATACATGGGTCTCTGTAAT 1738  
 690 yLeuGlnGluAlaGlnThrLeuCysLeuGluAlaAspLysTyrGlyPhe 706  
 1739 GCATTTGGAATCCTAAATCTCATCTGCAACAGACAGAGAGACTTC 1788  
 707 GlyAlaThrThrTyrPheValPheGlnArgGlyProAlaHisIleThrSe 723  
 1789 GGGAGCCTCTGTGGAGATCTCAGTGGAGAGATAGCCCTGAGTGC 1838  
 723 rLeuGluProAlaLysLysLeuLysPheTyrGluAspGlnGlyLysPhe 740  
 1839 TCTGGATTCCTCAAGAAAGCTGAGTTCTATGAGATACACATCACCCTTC 1888  
 740 rAlaIleuLysTyrPheGluLeuAlaGlyLeuIleThrGlnCysMetAla 756  
 1889 CTCACCCCAAGTGGACAGAGATTAGCAACCTTATAATATTCATGACGAC 1938  
 757 TyrAspProGlyArgArgProSerPheArgAlaIleLeuArgAspLeuAs 773  
 1939 TATGAGCCCAATTTTCAGGCTGCTTCAGAGCTGATCCGATCTTTAA 1988  
 773 nGlyLeuIleThrSerAspTyrGluLeuLeuSerAspProThrProGlyI 790  
 1989 CACCGCTTACTCCAGATTATGACTACTACAGAA... AATGACATGC 2035  
 790 IeProSerProArg... AspGluLeuCysValAlaGlyValAlaGlnLeuTyr 805  
 2036 TACCAACATGAGATAGTGCCTTAGGCTTTCTGTGCT... TTT 2079  
 806 AlCysGlnAspProAlaIlePheGluGluArgHisLeuLysTyrIleSe 822  
 2080 GAAGACAGGGAGCCCTACACAGTTTGAAGAGAGACACTTAATTTCTACA 2129

822 rLeuLeuGlyLysGlyAsnPheGlySerValGluLeuCysArgTyrAsp 839  
 2130 CGAGCTTGCCAAAGTAACCTTCGGAGGTGTGAGATGTCCCTATGACC 2179  
 839 rLeuGlyAspAsnThrGlyProLeuValAlaValLysGlnLeuGlnHis 855  
 2180 CGCTGCAGCACAACACTGGCAGGTGTGCTGTGAGAAATCCACAGAC 2229  
 856 SerValProAspGlnGlnArgAspPheGlnArgGluIleGlnIleLeuLys 872  
 2230 AGCAGCAGAGAGACCTCCGAGACTTTGAGAGAGATCGAGATGAGACTGGA 2279  
 872 sAlaLeuHisSerAspPheIleValLysTyrArgGlyValSerTyrGlyP 889  
 2280 ATCCTTGCGACATGACAAACATGCTCAGTACAGAGAGAGCTCTACAGG 2329  
 889 rGlyArgGlnSerLeuArgLeuValMetGluTyrLeuProSerGlyCys 905  
 2330 CGGGTCGGGCAACTTAAGATTATATGAAATATTTCATATGGAAGT 2379  
 906 LeuArgAspLeuLeuGlnArgHisArg... GlyLeuHisThrAspArgIle 921  
 2380 TTACGAGACTATCTCCAAATTAAGAGAGATGATCAACAAATAC 2429  
 921 uLeuLeuPheAlaTyrGlnIleCysLysGlyMetGluTyrLeuGlyAla 938  
 2430 TCTCAATACATCTCTCAGATATGCAAGGCGCATGGAATATCTGTAGCA 2479  
 938 rArgCysValHisArgAspPheAlaAlaArgAsnIleLeuValGlnSer 954  
 2480 AAGGATATCCACAGGGGCTGSCACAGAGAGAAATATGTTGGTGAAT 2529  
 955 GluAlaHisValLysIleAlaAspPheGlyLeuAlaLysLeuLeuProle 971  
 2530 GAGAACAGGGTTAAATAGAGAGACTTCGATTAAACAAAGCTTCCCA 2579  
 971 uGlyLysAspTyrTyrValValArgGluProGlyLysInserProIlePhe 988  
 2580 GGACAAAGATCTCAAAAGTAAAGAGCCAGGGCAAGCCCATATCT 2629  
 988 rPtyrAlaProGluSerLeuSerAspAsnIlePheSerArgGlnSerAsp 1004  
 2630 GGTAGCCACTCAATCTTGACGAGAGCAAGTTTCTGTGCTCCAT 2679  
 1005 ValTyrSerPheGlyValValLeuTyrGluLeuPheThrTyrCysAspLys 1021  
 2680 GTGTGAGCTTGGAGTGTCTATACGAACTTTACATACATACAGAGAA 2729  
 1021 sSerCysSerProSerAlaGluPheLeuArgMetMetCylProGluArg 1038  
 2730 GAGTAAAGTCCACCCGTGGAATTTATCGAATGTGCAATATGAAC 2779  
 1038 lGlyProProLeuCys... ArgLeuLeuGluLeuLeuAlaGlyValArg 1053  
 2780 AAGGCAATGATGTCTTCATTTGATAGAGCTACTAAGAGAGAGAGGA 2829  
 1054 ArgLeuProProProProThrCysProThrGluValGlnGluLeuMetG 1070  
 2830 AGATTGCCAAGCCAGAGAGATGCCCAATGAGATTATGATGATCAGAC 2879  
 1070 nLeuCysTyrPalaProGlnHisAspArgProAlaPheAlaThrLeu 1087  
 2880 AGAGTGCCTGGAACAACAATGTGAGCCAGGCTCTCTTCAGGAGACCTTT 2929  
 1087 er 1087  
 2930 CG 2931  
 seq\_name: /cgcn2\_2/gcgdata/geneseq/geneseq.NA1995.DAT:085413  
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 XX